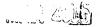SEQUENCE LISTING

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<110>   University of Texas Health Science Center at San Antonio
        Baseman, Joel
        Kannan, Thirumalai

<120>   METHODS AND COMPOSITIONS FOR MYCOPLASMA PNEUMONIAE EXOTOXINS

<130>   9237.10WO

<150>   US 60/508,607
<151>   2003-10-03

<160>   76

<170>   PatentIn version 3.2

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<213>   Mycoplasma pneumoniae

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Met Pro Asn Pro Val Arg Phe Val Tyr Arg Val Asp Leu Arg Ser Pro
1               5                   10                  15


Glu Glu Ile Phe Glu His Gly Phe Ser Thr Leu Gly Asp Val Arg Asn
            20                  25                  30


Phe Phe Glu His Ile Leu Ser Thr Asn Phe Gly Arg Ser Tyr Phe Ile
        35                  40                  45


Ser Thr Ser Glu Thr Pro Thr Ala Ala Ile Arg Phe Phe Gly Ser Trp
    50                  55                  60


Leu Arg Glu Tyr Val Pro Glu His Pro Arg Arg Ala Tyr Leu Tyr Glu
65                  70                  75                  80


Ile Arg Ala Asp Gln His Phe Tyr Asn Ala Arg Ala Thr Gly Glu Asn
                85                  90                  95


Leu Leu Asp Leu Met Arg Gln Arg Gln Val Val Phe Asp Ser Gly Asp
            100                 105                 110


Arg Glu Met Ala Gln Met Gly Ile Arg Ala Leu Arg Thr Ser Phe Ala
        115                 120                 125


Tyr Gln Arg Glu Trp Phe Thr Asp Gly Pro Ile Ala Ala Ala Asn Val
    130                 135                 140


Arg Ser Ala Trp Leu Val Asp Ala Val Pro Val Glu Pro Gly His Ala
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145                    150                    155                    160


His His Pro Ala Gly Arg Val Val Glu Thr Thr Arg Ile Asn Glu Pro
            165             170             175


Glu Met His Asn Pro His Tyr Gln Glu Leu Gln Thr Gln Ala Asn Asp
            180             185             190


Gln Pro Trp Leu Pro Thr Pro Gly Ile Ala Thr Pro Val His Leu Ser
            195             200             205


Ile Pro Gln Ala Ala Ser Val Ala Asp Val Ser Glu Gly Thr Ser Ala
    210             215             220


Ser Leu Ser Phe Ala Cys Pro Asp Trp Ser Pro Pro Ser Ser Asn Gly
225             230             235             240


Glu Asn Pro Leu Asp Lys Cys Ile Ala Glu Lys Ile Asp Asn Tyr Asn
            245             250             255


Leu Gln Ser Leu Pro Gln Tyr Ala Ser Ser Val Lys Glu Leu Glu Asp
            260             265             270


Thr Pro Val Tyr Leu Arg Gly Ile Lys Thr Gln Lys Thr Phe Met Leu
    275             280             285


Gln Ala Asp Pro Gln Asn Asn Asn Val Phe Leu Val Glu Val Asn Pro
    290             295             300


Lys Gln Lys Ser Ser Phe Pro Gln Thr Ile Phe Phe Trp Asp Val Tyr
305             310             315             320


Gln Arg Ile Cys Leu Lys Asp Leu Thr Gly Ala Gln Ile Ser Leu Ser
            325             330             335


Leu Thr Ala Phe Thr Thr Gln Tyr Ala Gly Gln Leu Lys Val His Leu
            340             345             350


Ser Val Ser Ala Val Asn Ala Val Asn Gln Lys Trp Lys Met Thr Pro
            355             360             365


Gln Asp Ile Ala Ile Thr Gln Phe Arg Val Ser Ser Glu Leu Leu Gly
    370             375             380


Gln Thr Glu Asn Gly Leu Phe Trp Asn Thr Lys Ser Gly Gly Ser Gln
385             390             395             400
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His Asp Leu Tyr Val Cys Pro Leu Lys Asn Pro Pro Ser Asp Leu Glu
              405             410             415


Glu Leu Gln Ile Ile Val Asp Glu Cys Thr Thr His Ala Gln Phe Val
              420             425             430


Thr Met Arg Ala Ala Ser Thr Phe Phe Val Asp Val Gln Leu Gly Trp
          435             440             445


Tyr Trp Arg Gly Tyr Tyr Tyr Thr Pro Gln Leu Ser Gly Trp Ser Tyr
      450             455             460


Gln Met Lys Thr Pro Asp Gly Gln Ile Phe Tyr Asp Leu Lys Thr Ser
465             470             475             480


Lys Ile Phe Phe Val Gln Asp Asn Gln Asn Val Phe Phe Leu His Asn
              485             490             495


Lys Leu Asn Lys Gln Thr Gly Tyr Ser Trp Asp Trp Val Glu Trp Leu
          500             505             510


Lys His Asp Met Asn Glu Asp Lys Asp Glu Asn Phe Lys Trp Tyr Phe
          515             520             525


Ser Arg Asp Asp Leu Thr Ile Pro Ser Val Glu Gly Leu Asn Phe Arg
      530             535             540


His Ile Arg Cys Tyr Ala Asp Asn Gln Gln Leu Lys Val Ile Ile Ser
545             550             555             560


Gly Ser Arg Trp Gly Gly Trp Tyr Ser Thr Tyr Asp Lys Val Glu Ser
          565             570             575


Asn Val Glu Asp Lys Ile Leu Val Lys Asp Gly Phe Asp Arg Phe
          580             585             590
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<212>  PRT
<213>  Mycoplasma pneumoniae

<400>  2

Met Pro Asn Pro Val Arg Phe Val Tyr Arg Val Asp Leu Arg Ser Pro
1           5               10              15
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Glu Glu Ile Phe Glu His Gly Phe Ser Thr Leu Gly Asp Val Arg Asn
            20                  25                  30

Phe Phe Glu His Ile Pro Ser Thr Asn Phe Gly Arg Ser Tyr Phe Ile
            35                  40                  45

Ser Thr Ser Glu Thr Pro Thr Ala Ala Ile Arg Phe Phe Gly Ser Trp
            50                  55                  60

Leu Arg Glu Tyr Val Pro Glu His Pro Arg Arg Ala Tyr Leu Tyr Glu
65              70                  75                  80

Ile Arg Ala Asp Gln His Phe Tyr Asn Ala Arg Ala Thr Gly Glu Asn
                85                  90                  95

Leu Leu Asp Leu Met Arg Gln Arg Gln Val Val Phe Asp Ser Gly Asp
                100                 105                 110

Arg Glu Met Ala Gln Met Gly Ile Arg Ala Leu Arg Thr Ser Phe Ala
            115                 120                 125

Tyr Gln Arg Glu Trp Phe Thr Asp Gly Pro Ile Ala Ala Ala Asn Val
    130                 135                 140

Arg Ser Ala Trp Leu Val Asp Ala Val Pro Val Glu Pro Gly His Ala
145                 150                 155                 160

His His Pro Ala Gly Arg Val Val Glu Thr Thr Arg Ile Asn Glu Pro
                165                 170                 175

Glu Met His Asn Pro His Tyr Gln Glu Leu Gln Thr Gln Ala Asn Asp
            180                 185                 190

Gln Pro Trp Leu Pro Thr Pro Gly Ile Ala Thr Pro Val His Leu Ser
        195                 200                 205

Ile Pro Gln Ala Ala Ser Val Ala Asp Val Ser Glu Gly Thr Ser Ala
    210                 215                 220

Ser Leu Ser Phe Ala Cys Pro Asp Trp Ser Pro Pro Ser Ser Asn Gly
225                 230                 235                 240

Glu Asn Pro Leu Asp Lys Cys Ile Ala Glu Lys Ile Asp Asn Tyr Asn
                245                 250                 255

Leu Gln Ser Leu Pro Gln Tyr Ala Ser Ser Val Lys Glu Leu Glu Asp
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4

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                  260                    265                    270


        Thr Pro Val Tyr Leu Arg Gly Ile Lys Thr Gln Lys Thr Phe Met Leu
                275                    280                    285


        Gln Ala Asp Pro Gln Asn Asn Asn Val Phe Leu Val Glu Val Asn Pro
                290                    295                    300


        Lys Gln Lys Ser Pro Phe Pro Gln Thr Ile Phe Phe Trp Asp Val Tyr
        305                    310                    315                    320


        Gln Arg Ile Cys Leu Lys Asp Leu Thr Gly Ala Gln Ile Ser Leu Ser
                        325                    330                    335
                                                                    :

        Leu Thr Ala Phe Thr Thr Gln Tyr Ala Gly Gln Leu Lys Val His Leu
                        340                    345                    350


        Ser Val Ser Ala Val Asn Ala Val Asn Gln Lys Trp Lys Met Thr Pro
                        355                    360                    365


        Gln Asp Ser Ala Ile Thr Gln Phe Arg Val Ser Ser Glu Leu Leu Gly
                370                    375                    380


        Gln Thr Glu Asn Gly Leu Ser Trp Asn Thr Lys Ser Gly Gly Ser Gln
        385                    390                    395                    400


        His Asp Leu Tyr Val Cys Pro Leu Lys Asn Pro Pro Ser Asp Leu Glu
                        405                    410                    415


        Glu Leu Gln Ile Ile Val Asp Glu Cys Thr Thr His Ala Gln Phe Val
                        420                    425                    430


        Thr Met Arg Ala Ala Ser Thr Phe Phe Val Asp Val Gln Leu Gly Trp
                        435                    440                    445


        Tyr Trp Arg Gly Tyr Tyr Tyr Thr Pro Gln Leu Ser Gly Trp Ser Tyr
                450                    455                    460


        Gln Met Lys Thr Pro Asp Gly Gln Ile Phe Tyr Asp Leu Lys Thr Ser
        465                    470                    475                    480


        Lys Ile Phe Phe Val Gln Asp Asn Gln Asn Val Phe Phe Leu His Asn
                        485                    490                    495


        Lys Leu Asn Lys Gln Thr Gly Tyr Ser Trp Asp Trp Val Glu Trp Leu
                        500                    505                    510
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Lys His Asp Met Asn Glu Asp Lys Asp Glu Asn Phe Lys Trp Tyr Phe
    515             520             525

Ser Arg Asp Asp Leu Thr Ile Pro Ser Val Glu Gly Leu Asn Phe Arg
    530             535             540

His Ile Arg Cys Tyr Ala Asp Asn Gln Gln Leu Lys Val Ile Ile Ser
545             550             555             560

Gly Ser Arg Trp Gly Gly Trp Tyr Ser Thr Tyr Asp Lys Val Glu Ser
            565             570             575

Asn Val Glu Asp Lys Ile Leu Val Lys Asp Gly Phe Asp Arg Phe
        580             585             590
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<211>  591
<212>  PRT
<213>  Mycoplasma pneumoniae

<400>  3
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Met Pro Asn Pro Val Arg Phe Val Tyr Arg Val Asp Leu Arg Ser Pro
1               5               10              15

Glu Glu Ile Phe Glu His Gly Phe Ser Thr Leu Gly Asp Val Arg Asn
            20              25              30

Phe Phe Glu His Ile Leu Ser Thr Asn Phe Gly Arg Ser Tyr Phe Ile
        35              40              45

Ser Thr Ser Glu Thr Pro Thr Ala Ala Ile Arg Phe Phe Gly Ser Trp
    50              55              60

Leu Arg Glu Tyr Val Pro Glu His Pro Arg Arg Ala Tyr Leu Tyr Glu
65              70              75              80

Ile Arg Ala Asp Gln His Phe Tyr Asn Ala Arg Ala Thr Gly Glu Asn
            85              90              95

Leu Leu Asp Leu Met Arg Gln Arg Gln Val Val Phe Asp Ser Gly Asp
            100             105             110

Arg Glu Met Ala Gln Met Gly Ile Arg Ala Leu Arg Thr Ser Phe Ala
    115             120             125
```

```
Tyr Gln Arg Glu Trp Phe Thr Asp Gly Pro Ile Ala Ala Ala Asn Val
    130                 135             140

Arg Ser Ala Trp Leu Val Asp Ala Val Pro Val Glu Pro Gly His Ala
145                 150             155                     160

His His Pro Ala Gly Arg Val Val Glu Thr Thr Arg Ile Asn Glu Pro
                165             170             175

Glu Met His Asn Pro His Tyr Gln Glu Leu Gln Thr Gln Ala Asn Asp
            180             185             190

Gln Pro Trp Leu Pro Thr Pro Gly Ile Ala Thr Pro Val His Leu Ser
        195             200             205

Ile Pro Gln Ala Ala Ser Val Ala Asp Val Ser Glu Gly Thr Ser Ala
    210             215             220

Ser Leu Ser Phe Ala Cys Pro Asp Trp Ser Pro Pro Ser Ser Asn Gly
225             230             235                     240

Glu Asn Pro Leu Asp Lys Cys Ile Ala Glu Lys Ile Asp Asn Tyr Asn
            245             250             255

Leu Gln Ser Leu Pro Gln Tyr Ala Ser Ser Val Lys Glu Leu Glu Asp
            260             265             270

Thr Pro Val Tyr Leu Arg Gly Ile Lys Thr Gln Lys Thr Phe Met Leu
        275             280             285

Gln Ala Asp Pro Gln Asn Asn Asn Val Phe Leu Val Glu Val Asn Pro
    290             295             300

Lys Gln Lys Ser Ser Phe Pro Gln Thr Ile Phe Phe Trp Asp Val Tyr
305             310             315                     320

Gln Arg Ile Cys Leu Lys Asp Leu Thr Gly Ala Gln Ile Ser Leu Ser
            325             330             335

Leu Thr Ala Phe Thr Thr Gln Tyr Ala Gly Gln Leu Lys Val His Leu
            340             345             350

Ser Val Ser Ala Val Asn Ala Val Asn Gln Lys Trp Lys Met Thr Pro
        355             360             365

Gln Asp Ser Ala Ile Thr Gln Phe Arg Val Ser Ser Glu Leu Leu Gly
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           370                   375                   380


Gln Thr Glu Asn Gly Leu Phe Trp Asn Thr Lys Ser Gly Gly Ser Gln
385                 390             395                 400


His Asp Leu Tyr Val Cys Pro Leu Lys Asn Pro Pro Ser Asp Leu Glu
                405             410                 415


Glu Leu Gln Ile Ile Val Asp Glu Cys Thr Thr His Ala Gln Phe Val
            420             425                 430


Thr Met Arg Ala Ala Ser Thr Phe Phe Val Asp Val Gln Leu Gly Trp
        435             440             445


Tyr Trp Arg Gly Tyr Tyr Tyr Thr Pro Gln Leu Ser Gly Trp Ser Tyr
    450             455             460


Gln Met Lys Thr Pro Asp Gly Gln Ile Phe Tyr Asp Leu Lys Thr Ser
465                 470             475                 480


Lys Ile Phe Phe Val Gln Asp Asn Gln Asn Val Phe Phe Leu His Asn
            485             490             495


Lys Leu Asn Lys Gln Thr Gly Tyr Ser Trp Asp Trp Val Glu Trp Leu
        500             505             510


Lys His Asp Met Asn Glu Asp Lys Asp Glu Asn Phe Lys Trp Tyr Phe
        515             520             525


Ser Arg Asp Asp Leu Thr Ile Pro Ser Val Glu Gly Leu Asn Phe Arg
    530             535             540


His Ile Arg Cys Tyr Ala Asp Asn Gln Gln Leu Lys Val Ile Ile Ser
545             550             555                 560


Gly Ser Arg Trp Gly Gly Trp Tyr Ser Thr Tyr Asp Lys Val Glu Ser
            565             570             575


Asn Val Glu Asp Lys Ile Leu Val Lys Asp Gly Phe Asp Arg Phe
            580             585             590


<210>  4
<211>  591
<212>  PRT
<213>  Mycoplasma pneumoniae

<400>  4
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Met Pro Asn Pro Val Arg Phe Val Tyr Arg Val Asp Leu Arg Ser Pro
1               5               10              15

Glu Glu Ile Phe Glu His Gly Phe Ser Thr Leu Gly Asp Val Arg Asn
            20              25              30

Phe Phe Glu His Ile Leu Ser Thr Asn Phe Gly Arg Ser Tyr Phe Ile
        35              40              45

Ser Thr Ser Glu Thr Pro Thr Ala Ala Ile Arg Phe Phe Gly Ser Trp
        50              55              60

Leu Arg Glu Tyr Val Pro Glu His Pro Arg Arg Ala Tyr Leu Tyr Glu
65              70              75              80

Ile Arg Ala Asp Gln His Phe Tyr Asn Ala Arg Ala Thr Gly Glu Asn
            85              90              95

Leu Leu Asp Leu Met Arg Gln Arg Gln Val Val Phe Asp Ser Gly Asp
            100             105             110

Arg Glu Met Ala Gln Met Gly Ile Arg Ala Leu Arg Thr Ser Phe Ala
        115             120             125

Tyr Gln Arg Glu Trp Phe Thr Asp Gly Pro Ile Ala Ala Ala Asn Val
    130             135             140

Arg Ser Ala Trp Leu Val Asp Ala Val Pro Val Glu Pro Gly His Ala
145             150             155             160

His His Pro Ala Gly Arg Val Val Glu Thr Thr Arg Ile Asn Glu Pro
            165             170             175

Glu Met His Asn Pro His Tyr Gln Glu Leu Gln Thr Gln Ala Asn Asp
            180             185             190

Gln Pro Trp Leu Pro Thr Pro Gly Ile Ala Thr Pro Val His Leu Ser
        195             200             205

Ile Pro Gln Ala Ala Ser Val Ala Asp Val Ser Glu Gly Thr Ser Ala
    210             215             220

Ser Leu Ser Phe Ala Cys Pro Asp Trp Ser Pro Pro Ser Ser Asn Gly
225             230             235             240
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Glu Asn Pro Leu Asp Lys Cys Ile Ala Glu Lys Ile Asp Asn Tyr Asn
                245   250   255

Leu Gln Ser Leu Pro Gln Tyr Ala Ser Ser Val Lys Glu Leu Glu Asp
                260   265   270

Thr Pro Val Tyr Leu Arg Gly Ile Lys Thr Gln Lys Thr Phe Met Leu
            275   280   285

Gln Ala Asp Pro Gln Asn Asn Asn Val Phe Leu Val Glu Val Asn Pro
        290   295   300

Lys Gln Lys Ser Ser Phe Pro Gln Thr Ile Phe Phe Trp Asp Val Tyr
305   310   315   320

Gln Arg Ile Cys Leu Lys Asp Leu Thr Gly Ala Gln Ile Ser Leu Ser
                325   330   335

Leu Thr Ala Phe Thr Thr Gln Tyr Ala Gly Gln Leu Lys Val His Leu
                340   345   350

Ser Val Ser Ala Val Asn Ala Val Asn Gln Lys Trp Lys Met Thr Pro
            355   360   365

Gln Asp Ser Ala Ile Thr Gln Phe Arg Val Ser Ser Glu Leu Leu Gly
        370   375   380

Gln Thr Glu Asn Gly Leu Phe Arg Asn Thr Lys Ser Gly Gly Ser Gln
385   390   395   400

His Asp Leu Tyr Val Cys Pro Leu Lys Asn Pro Pro Ser Asp Leu Glu
                405   410   415

Glu Leu Gln Ile Ile Val Asp Glu Cys Thr Thr His Ala Gln Phe Val
                420   425   430

Thr Met Arg Ala Ala Ser Thr Phe Phe Val Asp Val Gln Leu Gly Trp
            435   440   445

Tyr Trp Arg Gly Tyr Tyr Tyr Thr Pro Gln Leu Ser Gly Trp Ser Tyr
            450   455   460

Gln Met Lys Thr Pro Asp Gly Gln Ile Phe Tyr Asp Leu Lys Thr Ser
465   470   475   480

Lys Ile Phe Phe Val Gln Asp Asn Gln Asn Val Phe Phe Leu His Asn

                    485   490   ·   495

          Lys Leu Asn Lys Gln Thr Gly Tyr Ser Trp Asp Trp Val Glu Trp Leu
                  500   505   510

          Lys His Asp Met Asn Glu Asp Lys Asp Glu Asn Phe Lys Trp Tyr Phe
                  515   520   525

·   Ser Arg Asp Asp Leu Thr Ile Pro Ser Val Glu Gly Leu Asn Phe Arg
              530   535   540

          His Ile Arg Cys Tyr Ala Asp Asn Gln Gln Leu Lys Val Ile Ile Ser
          545   550   555   560

          Gly Ser Arg Trp Gly Gly Trp Tyr Ser Thr Tyr Asp Lys Val Glu Ser
                          565   570   575

          Asn Val Glu Asp Lys Ile Leu Val Lys Asp Gly Phe Asp Arg Phe
                      580   585   590

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          <212> PRT
          <213> Mycoplasma pneumoniae

          <400> 5

          Met Pro Asn Pro Val Arg Phe Val Tyr Arg Val Asp Leu Arg Ser Pro
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          Glu Glu Ile Phe Glu His Gly Phe Ser Thr Leu Gly Asp Val Arg Asn
                          20   25   30

          Phe Phe Glu His Ile Leu Ser Thr Asn Phe Gly Arg Ser Tyr Phe Ile
                      35   40   45

          Ser Thr Ser Glu Thr Pro Thr Ala Ala Ile Arg Phe Phe Gly Ser Trp
                  50   55   60

          Leu Arg Glu Tyr Val Pro Glu His Pro Arg Arg Ala Tyr Leu Tyr Glu
          65   70   75   80

          Ile Arg Ala Asp Gln His Phe Tyr Asn Ala Arg Ala Thr Gly Glu Asn
                          85   90   95

          Leu Leu Asp Leu Met Arg Gln Arg Gln Val Val Phe Asp Ser Gly Asp
                          100   105   110

```
Arg Glu Met Ala Gln Met Gly Ile Arg Ala Leu Arg Thr Ser Phe Ala
        115                 120                 125


Tyr Gln Arg Glu Trp Phe Thr Asp Gly Pro Ile Ala Ala Ala Asn Val
        130                 135                 140


Arg Ser Ala Trp Leu Val Asp Ala Val Pro Val Glu Pro Gly His Ala
145                 150                 155                 160


His His Pro Ala Gly Arg Val Val Glu Thr Thr Arg Ile Asn Glu Pro
                165                 170                 175


Glu Met His Asn Pro His Tyr Gln Glu Leu Gln Thr Gln Ala Asn Asp
                180                 185                 190


Gln Pro Trp Leu Pro Thr Pro Gly Ile Ala Thr Pro Val His Leu Ser
            195                 200                 205


Ile Pro Gln Ala Ala Ser Val Ala Asp Val Ser Glu Gly Thr Ser Ala
    210                 215                 220


Ser Leu Ser Phe Ala Cys Pro Asp Trp Ser Pro Pro Ser Ser Asn Gly
225                 230                 235                 240


Glu Asn Pro Leu Gly Lys Cys Ile Ala Glu Lys Ile Asp Asn Tyr Asn
                245                 250                 255


Leu Gln Ser Leu Pro Gln Tyr Ala Ser Ser Val Lys Glu Leu Glu Asp
                260                 265                 270


Thr Pro Val Tyr Leu Arg Gly Ile Lys Thr Gln Lys Thr Phe Met Leu
        275                 280                 285


Gln Ala Asp Pro Gln Asn Asn Asn Val Phe Leu Val Glu Val Asn Pro
    290                 295                 300


Lys Gln Lys Ser Ser Phe Pro Gln Thr Ile Phe Phe Trp Asp Val Tyr
305                 310                 315                 320


Gln Arg Ile Cys Leu Lys Asp Leu Thr Gly Ala Gln Ile Ser Leu Ser
                325                 330                 335


Leu Thr Ala Phe Thr Thr Gln Tyr Ala Gly Gln Leu Lys Val His Leu
            340                 345                 350
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Ser Val Ser Ala Val Asn Ala Val Asn Gln Lys Trp Lys Met Thr Pro
        355             360             365

Gln Asp Ser Ala Ile Thr Gln Phe Arg Val Ser Ser Glu Leu Leu Gly
    370             375             380

Gln Thr Glu Asn Gly Leu Phe Trp Asn Thr Lys Ser Gly Gly Ser Gln
385             390             395             400

His Asp Leu Tyr Val Cys Pro Leu Lys Asn Pro Pro Ser Asp Leu Glu
            405             410             415

Glu Leu Gln Ile Ile Val Asp Glu Cys Thr Thr His Ala Gln Phe Val
            420             425             430

Thr Met Arg Ala Ala Ser Thr Phe Phe Val Asp Val Gln Leu Gly Trp
        435             440             445

Tyr Trp Arg Gly Tyr Tyr Tyr Thr Pro Gln Leu Ser Gly Trp Ser Tyr
    450             455             460

Gln Met Lys Thr Pro Asp Gly Gln Ile Phe Tyr Asp Leu Lys Thr Ser
465             470             475             480

Lys Ile Phe Phe Val Gln Asp Asn Gln Asn Val Phe Phe Leu His Asn
            485             490             495

Lys Leu Asn Lys Gln Thr Gly Tyr Ser Trp Asp Trp Val Glu Trp Leu
        500             505             510

Lys His Asp Met Asn Glu Asp Lys Asp Glu Asn Phe Lys Trp Tyr Phe
    515             520             525

Ser Arg Asp Asp Leu Thr Ile Pro Ser Val Glu Gly Leu Asn Phe Arg
    530             535             540

His Ile Arg Cys Tyr Ala Asp Asn Gln Gln Leu Lys Val Ile Ile Ser
545             550             555             560

Gly Ser Arg Trp Gly Gly Trp Tyr Ser Thr Tyr Asp Lys Val Glu Ser
            565             570             575

Asn Val Glu Asp Lys Ile Leu Val Lys Asp Gly Phe Asp Arg Phe
            580             585             590
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<213> Artificial

<220>
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Met Pro Asn Pro Val Arg Phe Val Tyr Arg Val Asp Leu Arg Ser Pro
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Glu Glu Ile Phe Glu His Gly Phe Ser Thr Leu Gly Asp Val Arg Asn
            20   25   30

Phe Phe Glu His Ile Pro Ser Thr Asn Phe Gly Arg Ser Tyr Phe Ile
            35   40   45

Ser Thr Ser Glu Thr Pro Thr Ala Ala Ile Arg Phe Phe Gly Ser Trp
        50   55   60

Leu Arg Glu Tyr Val Pro Glu His Pro Arg Arg Ala Tyr Leu Tyr Glu
65   70   75   80

Ile Arg Ala Asp Gln His Phe Tyr Asn Ala Arg Ala Thr Gly Glu Asn
                85   90   95

Leu Leu Asp Leu Met Arg Gln Arg Gln Val Val Phe Asp Ser Gly Asp
            100   105   110

Arg Glu Met Ala Gln Met Gly Ile Arg Ala Leu Arg Thr Ser Phe Ala
            115   120   125

Tyr Gln Arg Glu Trp Phe Thr Asp Gly Pro Ile Ala Ala Ala Asn Val
        130   135   140

Arg Ser Ala Trp Leu Val Asp Ala Val Pro Val Glu Pro Gly His Ala
145   150   155   160

His His Pro Ala Gly Arg Val Val Glu Thr Thr Arg Ile Asn Glu Pro
                165   170   175

Glu Met His Asn Pro His Tyr Gln Glu Leu Gln Thr Gln Ala Asn Asp
                180   185   190

Gln Pro Trp Leu Pro Thr Pro Gly Ile Ala Thr Pro Val His Leu Ser
        195   200   205

```
Ile Pro Gln Ala Ala Ser Val Ala Asp Val Ser Glu Gly Thr Ser Ala
    210             215             220

Ser Leu Ser Phe Ala Cys Pro Asp Trp Ser Pro Pro Ser Ser Asn Gly
225             230             235             240

Glu Asn Pro Leu Gly Lys Cys Ile Ala Glu Lys Ile Asp Asn Tyr Asn
            245             250             255

Leu Gln Ser Leu Pro Gln Tyr Ala Ser Ser Val Lys Glu Leu Glu Asp
            260             265             270

Thr Pro Val Tyr Leu Arg Gly Ile Lys Thr Gln Lys Thr Phe Met Leu
        275             280             285

Gln Ala Asp Pro Gln Asn Asn Asn Val Phe Leu Val Glu Val Asn Pro
    290             295             300

Lys Gln Lys Pro Ser Phe Pro Gln Thr Ile Phe Phe Trp Asp Val Tyr
305             310             315             320

Gln Arg Ile Cys Leu Lys Asp Leu Thr Gly Ala Gln Ile Ser Leu Ser
            325             330             335

Leu Thr Ala Phe Thr Thr Gln Tyr Ala Gly Gln Leu Lys Val His Leu
            340             345             350

Ser Val Ser Ala Val Asn Ala Val Asn Gln Lys Trp Lys Met Thr Pro
        355             360             365

Gln Asp Ser Ala Ile Thr Gln Phe Arg Val Ser Ser Glu Leu Leu Gly
    370             375             380

Gln Thr Glu Asn Gly Leu Ser Arg Asn Thr Lys Ser Gly Gly Ser Gln
385             390             395             400

His Asp Leu Tyr Val Cys Pro Leu Lys Asn Pro Pro Ser Asp Leu Glu
            405             410             415

Glu Leu Gln Ile Ile Val Asp Glu Cys Thr Thr His Ala Gln Phe Val
            420             425             430

Thr Met Arg Ala Ala Ser Thr Phe Phe Val Asp Val Gln Leu Gly Trp
        435             440             445

Tyr Trp Arg Gly Tyr Tyr Tyr Thr Pro Gln Leu Ser Gly Trp Ser Tyr
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            450                    455                    460


Gln Met Lys Thr Pro Asp Gly Gln Ile Phe Tyr Asp Leu Lys Thr Ser
465                 470             475                 480


Lys Ile Phe Phe Val Gln Asp Asn Gln Asn Val Phe Phe Leu His Asn
                485             490                 495


Lys Leu Asn Lys Gln Thr Gly Tyr Ser Trp Asp Trp Val Glu Trp Leu
            500             505             510


Lys His Asp Met Asn Glu Asp Lys Asp Glu Asn Phe Lys Trp Tyr Phe
        515             520             525


Ser Arg Asp Asp Leu Thr Ile Pro Ser Val Glu Gly Leu Asn Phe Arg
    530             535             540


His Ile Arg Cys Tyr Ala Asp Asn Gln Gln Leu Lys Val Ile Ile Ser
545             550             555                 560


Gly Ser Arg Trp Gly Gly Trp Tyr Ser Thr Tyr Asp Lys Val Glu Ser
            565             570                 575


Asn Val Glu Asp Lys Ile Leu Val Lys Asp Gly Phe Asp Arg Phe
            580             585             590
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gagaaatttc tttgaacaca ttctctccac taattttggt agaagctatt ttatttccac       180

ttcagaaaca cccacagcag ctattcgctt ctttggtagc tggttacggg aatatgtacc       240

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ccgcgccact ggggagaact tgttagattt aatgcgtcaa agacaagtag tatttgactc       360

tggtgatcga gaaatggcac aaatgggaat tagagcttta cgcacttcct ttgcgtatca       420

acgtgaatgg tttaccgatg gtccaattgc agcagctaat gtccgtagtg cttgactagt       480

agatgctgtt cccgttgaac ctggtcatgc tcaccacccg gctggtcgtg ttgtagagac       540

tactagaatt aatgaaccgg aaatgcacaa ccctcattat caagagctgc aaacccaagc       600
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caatgatcaa ccatgattgc caacaccagg aatagctact cctgtacatt tatcaattcc    660

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aaagattgat aactataacc tacaatcctt accacagtac gctagcagtg taaaggaact    840

ggaagataca ccagtatacc taaggggaat taaaacgcaa aaaacctttá tgttacaagc    900

agatccgcaa aataacaatg tcttttttggt cgaagtaaac cccaaacaaa agtccagctt    960

tccccaaacc atcttctttt gggatgttta tcaacgaatt tgtctcaagg atttaactgg   1020

tgcacaaatc agtctttcgc ttactgcctt tactactcag tatgctggtc agctcaaagt   1080

gcaccttagt gttagcgcgg ttaatgccgt gaaccaaaag tgaaaaatga caccgcaaga   1140

cattgcaata actcagtttc gggtctcctc tgaactgtta ggtcaaactg aaaatggctt   1200

gttctgaaat accaagagtg gtggttcaca acacgatttg tatgtatgtc ctttgaaaaa   1260

tccacctagt gatttggaag aattacaaat aattgttgat gaatgtacta cccatgcgca   1320

gtttgttact atgcgtgcag ctagcacctt ctttgttgat gttcagctag ctggtattg   1380

aaggggttat tactataccc cacaattaag tggttgatct tatcagatga aaacaccaga   1440

tggacagata ttctatgatc taaaaacttc gaaaatcttc tttgtccagg acaaccaaaa   1500

cgtgttcttt ctccataata aactcaacaa acaaactggt tacagctggg attgagtaga   1560

atggctaaaa catgacatga atgaggacaa agacgaaaac tttaaatggt acttttcgcg   1620

tgatgacctt accattcctt ccgttgaagg gcttaacttc cgccacattc gctgttacgc   1680

tgacaaccag cagttaaagg tgatcataag cggttcacgt tggggcggtt ggtactccac   1740

ttacgataaa gttgaaagta atgtcgaaga taagattttg gtcaaagatg gttttgatcg   1800

cttttagcga ttaagcttta acgtcactgt tttgctctaa tgttagaagc aaagatcttg   1860
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<210> 8
<211> 1773
<212> DNA
<213> Artificial

<220>
<223> S1 nucleotide sequence with tga codons changed to tgg for
      expression in E. coli

<400> 8
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atgccaaatc ctgttagatt tgtttaccgt gttgatttga gaagccctga agaaattttt     60

gaacatggct tttcaacttt aggtgatgtg agaaatttct ttgaacacat tccctccact    120

aattttggta gaagctattt tatttccact tcagaaacac ccacagcagc tattcgcttc    180

tttggtagct ggttacggga atatgtacca gagcacccca gaagggctta cttatatgaa    240
```

17

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attcgtgccg accaacactt ttacaatgcc cgcgccactg gggagaactt gttagattta     300

atgcgtcaaa gacaagtagt atttgactct ggtgatcgag aaatggcaca aatgggaatt     360

agagctttac gcacttcctt tgcgtatcaa cgtgaatggt ttaccgatgg tccaattgca     420

gcagctaatg tccgtagtgc ttggctagta gatgctgttc ccgttgaacc tggtcatgct     480

caccacccgg ctggtcgtgt tgtagagact actagaatta atgaaccgga aatgcacaac     540

cctcattatc aagagctgca aacccaagcc aatgatcaac catggttgcc aacaccagga     600

atagctactc ctgtacattt atcaattccc caagcagctt ccgttgctga tgtttcggaa     660

ggtacttccg cttcgctatc gtttgcgtgc cctgattgga gtccaccttc tagtaatggt     720

gaaaatccgc tagacaaatg cattgcggaa aagattgata actataacct acaatcctta     780

ccacagtacg ctagcagtgt aaaggaactg gaagatacac cagtatacct aaggggaatt     840

aaaacgcaaa aaacctttat gttacaagca gatccgcaaa ataacaatgt cttttttggtc    900

gaagtaaacc ccaaacaaaa gcccagcttt ccccaaacca tcttcttttg ggatgtttat     960

caacgaattt gtctcaagga tttaactggt gcacaaatca gtctttcgct tactgccttt    1020

actactcagt atgctggtca gctcaaagtg caccttagtg ttagcgcggt taatgccgtg    1080

aaccaaaagt ggaaaatgac accgcaagac agtgcaataa ctcagtttcg ggtctcctct    1140

gaactgttag gtcaaactga aaatggcttg tcctggaata ccaagagtgg tggttcacaa    1200

cacgatttgt atgtatgtcc tttgaaaaat ccacctagtg atttggaaga attacaaata    1260

attgttgatg aatgtactac ccatgcgcag tttgttacta tgcgtgcagc tagcaccttc    1320

tttgttgatg ttcagctagg ctggtattgg aggggttatt actataccccc acaattaagt    1380

ggttggtctt atcagatgaa aacaccagat ggacagatat tctatgatct aaaaaacttcg   1440

aaaatcttct ttgtccagga caaccaaaac gtgttctttc tccataataa actcaacaaa    1500

caaactggtt acagctggga ttgggtagaa tggctaaaac atgacatgaa tgaggacaaa    1560

gacgaaaact ttaaatggta cttttcgcgt gatgacctta ccattccttc cgttgaaggg    1620

cttaacttcc gccacattcg ctgttacgct gacaaccagc agttaaaggt gatcataagc    1680

ggttcacgtt ggggcggttg gtactccact tacgataaag ttgaaagtaa tgtcgaagat    1740

aagattttgg tcaaagatgg ttttgatcgc ttt                                 1773
```

```
<210>   9
<211>   1773
<212>   DNA
<213>   Artificial

<220>
<223>   L2 nucleotide sequence with tga codons changed to tgg for
        expression in E. Coli
```

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<400>  9
atgccaaatc ctgttagatt tgtttaccgt gttgatttga gaagccctga agaaattttt      60
gaacatggct tttcaacttt aggtgatgtg agaaatttct ttgaacacat tctctccact     120
aattttggta gaagctattt tatttccact tcagaaacac ccacagcagc tattcgcttc     180
tttggtagct ggttacggga atatgtacca gagcacccca gaagggctta cttatatgaa     240
attcgtgccg accaacactt ttacaatgcc cgcgccactg gggagaactt gttagattta     300
atgcgtcaaa gacaagtagt atttgactct ggtgatcgag aaatggcaca aatgggaatt     360
agagctttac gcacttcctt tgcgtatcaa cgtgaatggt ttaccgatgg tccaattgca     420
gcagctaatg tccgtagtgc ttggctagta gatgctgttc ccgttgaacc tggtcatgct     480
caccacccgg ctggtcgtgt tgtagagact actagaatta atgaaccgga aatgcacaac     540
cctcattatc aagagctgca aacccaagcc aatgatcaac catggttgcc aacaccagga     600
atagctactc ctgtacattt atcaattccc caagcagctt ccgttgctga tgtttcggaa     660
ggtacttccg cttcgctatc gtttgcgtgc cctgattgga gtccaccttc tagtaatggt     720
gaaaatccgc taggcaaatg cattgcggaa aagattgata actataacct acaatcctta     780
ccacagtacg ctagcagtgt aaaggaactg gaagatacac cagtatacct aaggggaatt     840
aaaacgcaaa aaacctttat gttacaagca gatccgcaaa ataacaatgt cttttttggtc     900
gaagtaaacc ccaaacaaaa gtccagcttt ccccaaacca tcttcttttg ggatgtttat     960
caacgaattt gtctcaagga tttaactggt gcacaaatca gtctttcgct tactgccttt    1020
actactcagt atgctggtca gctcaaagtg caccttagtg ttagcgcggt taatgccgtg    1080
aaccaaaagt ggaaaatgac accgcaagac agtgcaataa ctcagtttcg ggtctcctct    1140
gaactgttag gtcaaactga aaatggcttg ttctggaata ccaagagtgg tggttcacaa    1200
cacgatttgt atgtatgtcc tttgaaaaat ccacctagtg atttggaaga attacaaata    1260
attgttgatg aatgtactac ccatgcgcag tttgttacta tgcgtgcagc tagcaccttc    1320
tttgttgatg ttcagctagg ctggtattgg aggggttatt actataccccc acaattaagt    1380
ggttggtctt atcagatgaa aacaccagat ggacagatat tctatgatct aaaaaacttcg    1440
aaaatcttct ttgtccagga caaccaaaac gtgttctttc tccataataa actcaacaaa    1500
caaactggtt acagctggga ttgggtagaa tggctaaaac atgacatgaa tgaggacaaa    1560
gacgaaaact ttaaatggta cttttcgcgt gatgacctta ccattccttc cgttgaaggg    1620
cttaacttcc gccacattcg ctgttacgct gacaaccagc agttaaaggt gatcataagc    1680
ggttcacgtt ggggcggttg gtactccact tacgataaag ttgaaagtaa tgtcgaagat    1740
aagattttgg tcaaagatgg ttttgatcgc ttt                                 1773
```

19

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<210>   10
<211>   1773
<212>   DNA
<213>   Artificial

<220>
<223>   JL nucleotide sequence with tga codons changed to tgg for
        expression in E. coli

<400>   10
atgccaaatc ctgttagatt tgtttaccgt gttgatttga gaagccctga agaaattttt      60

gaacatggct tttcaacttt aggtgatgtg agaaatttct ttgaacacat tctctccact     120

aattttggta gaagctattt tatttccact tcagaaacac ccacagcagc tattcgcttc     180

tttggtagct ggttacggga atatgtacca gagcacccca gaagggctta cttatatgaa     240

attcgtgccg accaacactt ttacaatgcc cgcgccactg gggagaactt gttagattta     300

atgcgtcaaa gacaagtagt atttgactct ggtgatcgag aaatggcaca aatgggaatt     360

agagctttac gcacttcctt tgcgtatcaa cgtgaatggt ttaccgatgg tccaattgca     420

gcagctaatg tccgtagtgc ttggctagta gatgctgttc ccgttgaacc tggtcatgct     480

caccacccgg ctggtcgtgt tgtagagact actagaatta atgaaccgga aatgcacaac     540

cctcattatc aagagctgca aacccaagcc aatgatcaac catggttgcc aacaccagga     600

atagctactc ctgtacattt atcaattccc caagcagctt ccgttgctga tgtttcggaa     660

ggtacttccg cttcgctatc gtttgcgtgc cctgattgga gtccaccttc tagtaatggt     720

gaaaatccgc tagacaaatg cattgcggaa aagattgata actataacct acaatcctta     780

ccacagtacg ctagcagtgt aaaggaactg gaagatacac cagtatacct aaggggaatt     840

aaaacgcaaa aaacctttat gttacaagca gatccgcaaa ataacaatgt cttttttggtc     900

gaagtaaacc ccaaacaaaa gtccagcttt ccccaaacca tcttcttttg ggatgtttat     960

caacgaattt gtctcaagga tttaactggt gcacaaatca gtctttcgct tactgccttt    1020

actactcagt atgctggtca gctcaaagtg caccttagtg ttagcgcggt taatgccgtg    1080

aaccaaaagt ggaaaatgac accgcaagac agtgcaataa ctcagtttcg ggtctcctct    1140

gaactgttag gtcaaactga aaatggcttg ttctggaata ccaagagtgg tggttcacaa    1200

cacgatttgt atgtatgtcc tttgaaaaat ccacctagtg atttggaaga attacaaata    1260

attgttgatg aatgtactac ccatgcgcag tttgttacta tgcgtgcagc tagcaccttc    1320

tttgttgatg ttcagctagg ctggtattgg aggggttatt actataccccc acaattaagt    1380

ggttggtctt atcagatgaa aacaccagat ggacagatat tctatgatct aaaaaacttcg    1440

aaaatcttct ttgtccagga caaccaaaac gtgttctttc tccataataa actcaacaaa    1500
```

```
caaactggtt acagctggga ttgggtagaa tggctaaaac atgacatgaa tgaggacaaa   1560   .

gacgaaaact ttaaatggta cttttcgcgt gatgacctta ccattccttc cgttgaaggg   1620

cttaacttcc gccacattcg ctgttacgct gacaaccagc agttaaaggt gatcataagc   1680

ggttcacgtt ggggcggttg gtactccact tacgataaag ttgaaagtaa tgtcgaagat   1740

aagattttgg tcaaagatgg ttttgatcgc ttt                                1773
```

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<210>  11
<211>  1773
<212>  DNA
<213>  Artificial

<220>
<223>  RJL1 nucleotide sequence with tga codons changed to tgg for
       expression in E. coli

<400>  11
atgccaaatc ctgttagatt tgtttaccgt gttgatttga gaagccctga agaaattttt     60

gaacatggct tttcaacttt aggtgatgtg agaaatttct ttgaacacat tctctccact    120

aattttggta gaagctattt tatttccact tcagaaacac ccacagcagc tattcgcttc    180

tttggtagct ggttacggga atatgtacca gagcacccca gaagggctta cttatatgaa    240

attcgtgccg accaacactt ttacaatgcc cgcgccactg gggagaactt gttagattta    300

atgcgtcaaa gacaagtagt atttgactct ggtgatcgag aaatggcaca atgggaatt     360

agagctttac gcacttcctt tgcgtatcaa cgtgaatggt ttaccgatgg tccaattgca    420

gcagctaatg tccgtagtgc cttggctagta gatgctgttc ccgttgaacc tggtcatgct    480

caccacccgg ctggtcgtgt tgtagagact actagaatta atgaaccgga aatgcacaac    540

cctcattatc aagagctgca aacccaagcc aatgatcaac catggttgcc aacaccagga    600

atagctactc ctgtacattt atcaattccc caagcagctt ccgttgctga tgtttcggaa    660

ggtacttccg cttcgctatc gtttgcgtgc cctgattgga gtccaccttc tagtaatggt    720

gaaaatccgc tagacaaatg cattgcggaa aagattgata actataacct acaatcctta    780

ccacagtacg ctagcagtgt aaaggaactg gaagatacac cagtatacct aaggggaatt    840

aaaacgcaaa aaaccttat gttacaagca gatccgcaaa ataacaatgt cttttttggtc    900

gaagtaaacc ccaaacaaaa gtccagcttt ccccaaacca tcttcttttg ggatgtttat    960

caacgaattt gtctcaagga tttaactggt gcacaaatca gtctttcgct tactgccttt   1020

actactcagt atgctggtca gctcaaagtg caccttagtg ttagcgcggt taatgccgtg   1080

aaccaaaagt ggaaaatgac accgcaagac agtgcaataa ctcagtttcg ggtctcctct   1140

gaactgttag gtcaaactga aaatggcttg ttccggaata ccaagagtgg tggttcacaa   1200
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cacgatttgt atgtatgtcc tttgaaaaat ccacctagtg atttggaaga attacaaata   1260

attgttgatg aatgtactac ccatgcgcag tttgttacta tgcgtgcagc tagcaccttc   1320

tttgttgatg ttcagctagg ctggtattgg aggggttatt actataccccc acaattaagt   1380

ggttggtctt atcagatgaa aacaccagat ggacagatat tctatgatct aaaaacttcg   1440

aaaatcttct ttgtccagga caaccaaaac gtgttctttc tccataataa actcaacaaa   1500

caaactggtt acagctggga ttgggtagaa tggctaaaac atgacatgaa tgaggacaaa   1560

gacgaaaact ttaaatggta cttttcgcgt gatgacctta ccattccttc cgttgaaggg   1620

cttaacttcc gccacattcg ctgttacgct gacaaccagc agttaaaggt gatcataagc   1680

ggttcacgtt ggggcggttg gtactccact tacgataaag ttgaaagtaa tgtcgaagat   1740

aagattttgg tcaaagatgg ttttgatcgc ttt                               1773
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<210>  12
<211>  24
<212>  DNA
<213>  Artificial

<220>
<223>  Oligonucleotide primer

<400>  12
tttttacata tgccaaatcc tgtt                                           24


<210>  13
<211>  28
<212>  DNA
<213>  Artificial

<220>
<223>  Oligonucleotide primer

<400>  13
cgttaaagga tcctcgctaa aagcgatc                                       28


<210>  14
<211>  25
<212>  DNA
<213>  Artificial

<220>
<223>  Oligonucleotide primer

<400>  14
ctagccaagc actacggaca ttagc                                          25


<210>  15
<211>  27
<212>  DNA
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```
<213>  Artificial

<220>
<223>  Oligonucleotide primer

<400>  15
cgtagtgctt ggctagtaga tgctgtt                                    27


<210>  16
<211>  23
<212>  DNA
<213>  Artificial

<220>
<223>  Oligonucleotide primer

<400>  16
cctggtgttg gcaaccatgg ttg                                        23


<210>  17
<211>  23
<212>  DNA
<213>  Artificial

<220>
<223>  Oligonucleotide primer

<400>  17
gatcaaccat ggttgccaac acc                                        23


<210>  18
<211>  24
<212>  DNA
<213>  Artificial

<220>
<223>  Oligonucleotide primer

<400>  18
aaggtggact ccaatcaggg cacg                                       24


<210>  19
<211>  24
<212>  DNA
<213>  Artificial

<220>
<223>  Oligonucleotide primer

<400>  19
cgtgccctga ttggagtcca cctt                                       24


<210>  20
<211>  23
<212>  DNA
<213>  Artificial
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```
<220>
<223>  Oligonucleotide primer

<400>  20
gcggtgtcat tttccacttt tgg                                    23


<210>  21
<211>  23
<212>  DNA
<213>  Artificial

<220>
<223>  Oligonucleotide primer

<400>  21
ccaaaagtgg aaaatgacac cgc                                    23


<210>  22
<211>  22
<212>  DNA
<213>  Artificial

<220>
<223>  Oligonucleotide primer

<400>  22
ggtattccag aacaagccat tt                                     22


<210>  23
<211>  24
<212>  DNA
<213>  Artificial

<220>
<223>  Oligonucleotide primer

<400>  23
gcttgttctg gaataccaag agtg                                   24


<210>  24
<211>  21
<212>  DNA
<213>  Artificial

<220>
<223>  Oligonucleotide primer

<400>  24
ataacccta taccagccta g                                       21


<210>  25
<211>  59
<212>  DNA
<213>  Artificial
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```
<220>
<223>  Oligonucleotide primer

<400>  25
gctggtattg gaggggttat tactatacc cacaattaag tggttggtct tatcagatg          59


<210>  26
<211>  24
<212>  DNA
<213>  Artificial

<220>
<223>  Oligonucleotide primer

<400>  26
ccattctacc caatcccagc tgta                                              24


<210>  27
<211>  24
<212>  DNA
<213>  Artificial

<220>
<223>  Oligonucleotide primer

<400>  27
tacagctggg attgggtaga atgg                                              24


<210>  28
<211>  24
<212>  DNA
<213>  Mycoplasma pneumoniae

<400>  28
tttttaaaaa tgccaaatcc tgtt                                              24


<210>  29
<211>  20
<212>  DNA
<213>  Mycoplasma pneumoniae

<400>  29
aatgtccgta gtgcttgact                                                   20


<210>  30
<211>  20
<212>  DNA
<213>  Artificial

<220>
<223>  Modified M129/B9 sequence

<400>  30
aatgtccgta gtgcttggct                                                   20
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<210>  31
<211>  20
<212>  DNA
<213>  Artificial

<220>
<223>  Oligonucleotide primer

<400>  31
agccaagcac tacggacatt                                                            20


<210>  32
<211>  22
<212>  DNA
<213>  Mycoplasma pneumoniae

<400>  32
tgcttgacta gtagatgctg tt                                                         22


<210>  33
<211>  22
<212>  DNA
<213>  Artificial

<220>
<223>  Oligonucleotide primer

<400>  33
tgcttggcta gtagatgctg tt                                                         22


<210>  34
<211>  18
<212>  DNA
<213>  Mycoplasma pneumoniae

<400>  34
atgattgcca acaccagg                                                              18


<210>  35
<211>  18
<212>  DNA
<213>  Artificial

<220>
<223>  Modified M129/B9 sequence

<400>  35
atggttgcca acaccagg                                                              18


<210>  36
<211>  18
<212>  DNA
<213>  Artificial

<220>
<223>  Oligonucleotide primer
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```
<400>  36
cctggtgttg gcaaccat                                                    18


<210>  37
<211>  18
<212>  DNA
<213>  Mycoplasma pneumoniae

<400>  37
accatgattg ccaacacc                                                    18


<210>  38
<211>  18
<212>  DNA
<213>  Artificial

<220>
<223>  Oligonucleotide primer

<400>  38
accatggttg ccaacacc                                                    18


<210>  39
<211>  19
<212>  DNA
<213>  Mycoplasma pneumoniae

<400>  39
cctgattgaa gtccacctt                                                   19


<210>  40
<211>  19
<212>  DNA
<213>  Artificial

<220>
<223>  Modified M129/B9 sequence

<400>  40
cctgattgga gtccacctt                                                   19


<210>  41
<211>  19
<212>  DNA
<213>  Artificial

<220>
<223>  Oligonucleotide primer

<400>  41
aaggtggact ccaatcagg                                                   19


<210>  42
<211>  18
```

```
<212>   DNA
<213>   Mycoplasma pneumoniae

<400>   42
cgtgccctga ttgaagtc                                              18


<210>   43
<211>   18
<212>   DNA
<213>   Artificial

<220>
<223>   Oligonucleotide primer

<400>   43
cgtgccctga ttggagtc                                              18


<210>   44
<211>   20
<212>   DNA
<213>   Mycoplasma pneumoniae

<400>   44
aaagtgaaaa atgacaccgc                                            20


<210>   45
<211>   20
<212>   DNA
<213>   Artificial

<220>
<223>   Modified M129/B9 sequence

<400>   45
aaagtggaaa atgacaccgc                                            20


<210>   46
<211>   20
<212>   DNA
<213>   Artificial

<220>
<223>   Oligonucleotide primer

<400>   46
gcggtgtcat tttccacttt                                            20


<210>   47
<211>   20
<212>   DNA
<213>   Mycoplasma pneumoniae

<400>   47
caaaagtgaa aaatgacacc                                            20
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```
<210>  48
<211>  20
<212>  DNA
<213>  Artificial

<220>
<223>  Oligonucleotide primer

<400>  48
caaaagtgga aaatgacacc                                          20


<210>  49
<211>  22
<212>  DNA
<213>  Mycoplasma pneumoniae

<400>  49
aaatggcttg ttctgaaata cc                                       22


<210>  50
<211>  22
<212>  DNA
<213>  Artificial

<220>
<223>  Modified M129/B9 sequence

<400>  50
aaatggcttg ttctggaata cc                                       22


<210>  51
<211>  23
<212>  DNA
<213>  Mycoplasma pneumoniae

<400>  51
gcttgttctg aaataccaag agt                                      23


<210>  52
<211>  23
<212>  DNA
<213>  Artificial

<220>
<223>  Oligonucleotide primer

<400>  52
gcttgttctg gaataccaag agt                                      23


<210>  53
<211>  20
<212>  DNA
<213>  Mycoplasma pneumoniae

<400>  53
taggctggta ttgaaggggt                                          20
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```
<210>  54
<211>  20
<212>  DNA
<213>  Artificial

<220>
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<400>  54
taggctggta ttggaggggt                                              20


<210>  55
<211>  17
<212>  DNA
<213>  Artificial

<220>
<223>  Oligonucleotide primer

<400>  55
acccctatac cagccta                                                 17


<210>  56
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Phe Phe Glu His Ile Leu Ser Thr Asn Phe Gly Arg Ser Tyr Phe Ile
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Ser Thr Ser Glu Thr Pro Thr Ala Ala Ile Arg Phe Phe Gly Ser Trp
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Leu Arg Glu Tyr Val Pro Glu His Pro Arg Arg Ala Tyr Leu Tyr Glu
65              70                  75                  80

Ile Arg Ala Asp Gln His Phe Tyr Asn Ala Arg Ala Thr Gly Glu Asn
            85                  90                  95

Leu Leu Asp Leu Met Arg Gln Arg Gln Val Val Phe Asp Ser Gly Asp
            100                 105                 110

Arg Glu Met Ala Gln Met Gly Ile Arg Ala Leu Arg Thr Ser Phe Ala
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Tyr Gln Arg Glu Trp Phe Thr Asp Gly Pro Ile Ala Ala Ala Asn Val
    130             135             140

Arg Ser Ala Trp Leu Val Asp Ala Val Pro Val Glu Pro Gly His Ala
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His His Pro Ala Gly Arg Val Val Glu Thr Thr Arg Ile Asn Glu Pro
            165             170             175

Glu Met His Asn Pro His Tyr Gln Glu Leu Gln Thr Gln Ala Asn Asp
            180             185             190

Gln Pro Trp Leu Pro Thr Pro Gly Ile Ala Thr Pro Val His Leu Ser
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Ile Pro Gln Ala Ala Ser Val Ala Asp Val Ser Glu Gly Thr Ser Ala
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Asn Pro Leu Asp Lys Cys Ile Ala Glu Lys Ile Asp Asn Tyr Asn Leu
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Gln Ser Leu Pro Gln Tyr Ala Ser Ser Val Lys Glu Leu Glu Asp Thr
65              70              75              80

Pro Val Tyr Leu Arg Gly Ile Lys Thr Gln Lys Thr Phe Met Leu Gln
            85              90              95

Ala Asp Pro Gln Asn Asn Asn Val Phe Leu Val Glu Val Asn Pro Lys
            100             105             110

Gln Lys Ser Ser Phe Pro Gln Thr Ile Phe Phe Trp Asp Val Tyr Gln
        115             120             125

Arg Ile Cys Leu Lys Asp Leu Thr Gly Ala Gln Ile Ser Leu Ser Leu
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Thr Ala Phe Thr Thr Gln Tyr Ala Gly Gln Leu Lys Val His Leu Ser
145             150             155             160

Val Ser Ala Val Asn Ala Val Asn Gln Lys Trp Lys Met Thr Pro Gln
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Asp Ile Ala Ile Thr Gln Phe Arg Val Ser Ser Glu Leu Leu Gly Gln
            180             185             190

Thr Glu Asn Gly Leu Phe Trp Asn Thr Lys Ser Gly Gly Ser Gln His
        195             200             205

Asp Leu Tyr Val Cys Pro Leu Lys Asn Pro Pro Ser Asp Leu Glu Glu
    210             215             220

Leu Gln Ile Ile Val Asp Glu Cys Thr Thr His Ala Gln Phe Val Thr
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Arg Val Ser Ser Glu Leu Leu Gly Gln Thr Glu Asn Gly Leu Phe Trp
        35                  40                  45


Asn Thr Lys Ser Gly Gly Ser Gln His Asp Leu Tyr Val Cys Pro Leu
    50                  55                  60


Lys Asn Pro Pro Ser Asp Leu Glu Glu Leu Gln Ile Ile Val Asp Glu
65                  70                  75                  80


Cys Thr Thr His Ala Gln Phe Val Thr Met Arg Ala Ala Ser Thr Phe
                85                  90                  95


Phe Val Asp Val Gln Leu Gly Trp Tyr Trp Arg Gly Tyr Tyr Tyr Thr
            100                 105                 110


Pro Gln Leu Ser Gly Trp Ser Tyr Gln Met Lys Thr Pro Asp Gly Gln
        115                 120                 125


Ile Phe Tyr Asp Leu Lys Thr Ser Lys Ile Phe Phe Val Gln Asp Asn
    130                 135                 140


Gln Asn Val Phe Phe Leu His Asn Lys Leu Asn Lys Gln Thr Gly Tyr
145                 150                 155                 160


Ser Trp Asp Trp Val Glu Trp Leu Lys His Asp Met Asn Glu Asp Lys
                165                 170                 175


Asp Glu Asn Phe Lys Trp Tyr Phe Ser Arg Asp Asp Leu Thr Ile Pro
            180                 185                 190
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Ser Val Glu Gly Leu Asn Phe Arg His Ile Arg Cys Tyr Ala Asp Asn
        195                 200             205


Gln Gln Leu Lys Val Ile Ile Ser Gly Ser Arg Trp Gly Gly Trp Tyr
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Ser Thr Tyr Asp Lys Val Glu Ser Asn Val Glu Asp Lys Ile Leu Val
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Lys Asp Gly Phe Asp Arg Phe
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aattttggta gaagctattt tatttccact tcagaaacac ccacagcagc tattcgcttc   180

tttggtagct ggttacggga atatgtacca gagcacccca gaagggctta cttatatgaa   240

attcgtgccg accaacactt ttacaatgcc cgcgccactg gggagaactt gttagattta   300

atgcgtcaaa gacaagtagt atttgactct ggtgatcgag aaatggcaca aatgggaatt   360
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caccacccgg ctggtcgtgt tgtagagact actagaatta atgaaccgga aatgcacaac   540

cctcattatc aagagctgca aacccaagcc aatgatcaac catggttgcc aacaccagga   600

atagctactc ctgtacattt atcaattccc caagcagctt ccgttgctga tgtttcggaa   660

ggtacttccg cttcgctatc gtttgcgtgc cctgattgga gtccaccttc tagtaatggt   720

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Arg Val Asp Leu Arg Ser Pro Glu Glu Ile Phe Glu His Gly Phe Ser
        35                  40                  45


Thr Leu Gly Asp Val Arg Asn Phe Phe Glu His Ile Leu Ser Thr Asn
    50                  55                  60


Phe Gly Arg Ser Tyr Phe Ile Ser Thr Ser Glu Thr Pro Thr Ala Ala
65                  70                  75                  80


Ile Arg Phe Phe Gly Ser Trp Leu Arg Glu Tyr Val Pro Glu His Pro
                85                  90                  95


Arg Arg Ala Tyr Leu Tyr Glu Ile Arg Ala Asp Gln His Phe Tyr Asn
                100                 105                 110


Ala Arg Ala Thr Gly Glu Asn Leu Leu Asp Leu Met Arg Gln Arg Gln
            115                 120                 125


Val Val Phe Asp Ser Gly Asp Arg Glu Met Ala Gln Met Gly Ile Arg
        130                 135                 140
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37

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Ala Leu Arg Thr Ser Phe Ala Tyr Gln Arg Glu Trp Phe Thr Asp Gly
145             150              155             160


Pro Ile Ala Ala Ala Asn Val Arg Ser Ala Trp Leu Val Asp Ala Val
            165              170             175


Pro Val Glu Pro Gly His Ala His His Pro Ala Gly Arg Val Val Glu
            180              185             190


Thr Thr Arg Ile Asn Glu Pro Glu Met His Asn Pro His Tyr Gln Glu
            195              200             205


Leu Gln Thr Gln Ala Asn Asp Gln Pro Trp Leu Pro Thr Pro Gly Ile
    210              215             220


Ala Thr Pro Val His Leu Ser Ile Pro Gln Ala Ala Ser Val Ala Asp
225             230              235             240


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<222>  (1749)..(1749)
<223>  n is a, c, g, or t

<220>
<221>  misc_feature
<222>  (1752)..(1752)
<223>  n is a, c, g, or t

<220>
<221>  misc_feature
<222>  (1761)..(1761)
<223>  n is a, c, g, or t

<220>
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<222>  (1770)..(1770)
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<223> n is a, c, g, or t

<400> 76

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ttyggnwsnt ggytnmgnga rtaygtnccn garcayccnm gnmgngcnta yytntaygar     240

athmgngcng aycarcaytt ytayaaygcn mgngcnacng gngaraayyt nytngayytn     300

atgmgncarm gncargtngt nttygaywsn ggngaymgng aratggcnca ratgggnath     360

mgngcnytnm gnacnwsntt ygcntaycar mgngartggt tyacngaygg nccnathgcn     420

gcngcnaayg tnmgnwsngc ntggytngtn gaygcngtnc cngtngarcc nggncaygcn     480

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athgcnacnc cngtncayyt nwsnathccn cargcngcnw sngtngcnga ygtnwsngar     660

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carmgnatht gyytnaarga yytnacnggn gcncarathw snytnwsnyt nacngcntty    1020

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garytnytng gncaracnga raayggnytn wsnmgnaaya cnaarwsngg nggnwsncar    1200

caygayytnt aygtntgycc nytnaaraay ccnccnwsng ayytngarga rytncarath    1260

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ttygtngayg tncarytngg ntggtaytgg mgnggntayt aytayacncc ncarytnwsn    1380

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